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354 KLKQAVKFLGEQ 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MANAX-Thompson B., Chaney W., Wing J.S., Gould S.J., Loper J.E.;

"Characterization of the pyoluteorin biosynthetic gene cluster of
"Deterior of the pyoluteorin biosynthetic gene cluster of
"In Bacteriol 181:2166-214(1999).

R Interpro: IPRO01227; Ac_transferase.

R Interpro: IPRO01294; Ketoacyl-synt.
R Interpro: IPRO01998; Phinlase.
R Pfam: PF00109; Ketoacyl-synt; 2.
R Pfam: PF00109; Ketoacyl-synt; 2.
R Pfam: PF00109; Ketoacyl-synt.
R Pfam: PF00550; pp-binding; 2.
R Pfam: PF00550; pp-binding; 2.
1:1: | 1|: :|1|: | 1|: 356 EVSEEDVHDMPYLKAVVLEGLRKHPPAHMLLPHKAAEDMDVGGYLIPKGTIVNFWVAEMG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                      Pseudomonas fluorescens.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 ELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGSQDGAG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.8%; Score 69.5; DB 2; Length 2458; 32.1%; Pred. No. 2.4e+02; Live 14; Mismatches 19; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nowak-Thompson B., Gould S.J., Loper J.E.;
"Identification and sequence analysis of the genes encoding a polyketide synthase required for pyoluteorin biosynthesis in Pseudomonas fluorescens Pf-5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262676 MW; AE756080AE1A5FB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09CFY4;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Fibronectin-binding protein.
                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Polyketide synthase type I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROSITE; PS00606; B_KETOACYL_SYNTHASE; 2.
ROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
ROSITE; PS00098; THIOLASE_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540 AA.
                                                                                                                                                                                                   2458 AA
                                                                                               416 RDEKEWEKPMEFMPERFLPGGDGEGVD 442
                                                       ------ DGAGTD 98
                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=PF-5;
MEDLINE=99194726; Pubmed=10094695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98094250; PubMed-9434161;
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                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 204:17-24(1997)
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas.
NCBI_TaxID=294;
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Q9CFY4
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051827
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STRAIN=IL1403;
MFDLINS=121316; PubMed=11337471;
BOLOtin A., Wincker P., Manger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).

EMBL; AE006365; AAK05425.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 DNDEFFM---DFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQP-MHKAE 80
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 12.7%; Score 69; DB 16; Length 540 Best Local Similarity 30.6%; Pred. No. 41; Matches 22; Conservative 9; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 540 AA; 61285 MW; 4DAC3CCBCF72867 CRC64;
                         Streptococcaceae; Lactococcus.NCBI_TaxID=1360;
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Search completed: May 14, 2003, 10:52:40 Job time : 37 secs

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[1]
SEQUENCE FROM N.A.
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Q9FW93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        potyviruses from sugarcane and maize in China."; 2002).
                                                                                                                Gaps
                                                                                                                                              2 KGSRALLLVALTLFCICRMATGEDNDEF----FMDFLQTLL-VGTPEELYEGTLGKYNVN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 TGEDNDEFFWDFLQT----LLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMH 77
                                                                                                                                                                                                                                                                                                                                                                                                                                Polyprotein.
Sorghum mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polyprotein.
Sorghum mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3071;
                                                                           DB 11; Length 500;
                                                                                                                                                                                                                                        57 E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSQDGAGTDY 99
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 COAT PROTEIN.
349970 MW; 2FD59A0668DE2FB7 CRC64;
SMART; SM00382; AAA; 1.
PROSITE; PS00300; SRP54; UNKNOWN_1.
SEQUENCE 500 AA; 55492 MW; C957B6F76C6A224B CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                              42;
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Pred. No. 2.5e+02;
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NIA-PRO PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P1 PROTEIN.
HC-PRO PROTEIN.
P3 PROTEIN.
                                                                         13.4%; Score 72.5; D
32.4%; Pred. No. 15;
Live 14; Mismatches
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CI PROTEIN.
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"Characterisation of potyviruses
Arch. Virol. 147:0-0(2002).
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33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAC84437.1;
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                                                                                          Local Similarity 32.4% tes 36; Conservative
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NCBI_TaxID=32619;
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1988
2230
2751
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EMBL; AJ310197
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SEQUENCE
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                                                                           Query Match
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Matches
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Chen J., Chen J.P., Adams M.J.;
"Characterisation of potyviruses from sugarcane and maize in China.";
Arch. Virol. 147:0-0(2002).
EMBL. AJ310198; CAC84438.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C., Hsiao J., Zismann V., Pai G., Bowman C.L., Fujil C.Y., VanAken S.E., Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V., Quackenbush J., White O., Sallberg S.L., Fraser C.M.; "Oryza sativa chromosome 10 BAC OSJNBa0026L12 genomic sequence."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         22 TGEDNDEFFMDFLQT----LLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMH 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GSRALLLVALTLFCICRMATGEDNDEFFMDFLQTLLVGTP----EELYE-----GTLGKY 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 NVNEDAKAAMTELKSCI-DGLQ---PMH-------KAELVKLLVQVLG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                Length 3071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 643;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                           E3D326DE1B9ACB05 CRC64;
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SEQUENCE 643 AA; 70706 MW; C695CA5DF1A36463 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                          13.0%; Score 70.5; DB 12; 33.3%; Pred. No. 2.5e+02; ive 10; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
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                                                                                                     P1 PROTEIN.
P2-PRO PROTEIN.
P3 PROTEIN.
6K1 PROTEIN.
C1 PROTEIN.
6K2 PROTEIN.
NIA-VPG PROTEIN.
                                                                                                                                                                                                                                               NIA-PRO PROTEIN.
NIB PROTEIN.
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PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.8%; Score 69.5; DB
22.4%; Pred. No. 45;
tive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           643 AA
                                                                                                                                                                                                                                                                                      COAT PROTEIN
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InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                         349537 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative cytochrome P450.
OSJNBA0026L12.20.
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                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                    1745
1798
1987
                                                                                                                                                                                                                                             2229
2750
3071
                                                                                                                                                                1107
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                                                                                                                                                                                                                                                                                                         3071 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2410 KTEANK 2415
                                                                                                                                                                  1041
                                                                                                                                                                                                       1746
1799
1988
2230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 KAELVK 83
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63 KECTDEIDKGKRVLIAAVLTKIV

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3
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LLLVALTLFCICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTEL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 CICRMATGEDNDEFFMDFLQTLLVGTP-----EELYEGTLG-KYNVNEDAKAAMTELKSC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                               4 CICQFSVRVPKD-----IHTDTVGHPPVLISELVLQCTRGTNYVLTEESS---TICKKC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                           13.7%; Score 74; DB 5; Length 457; 27.2%; Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.5%; Score 73; DB 6; Length 90; 27.7%; Pred. No. 1.5; tive 15; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-LACRIMAL GLAND;
TISSUE-LACRIMAL GLAND;
Thao C., Nguyen T.X., Lehrer R.I.;
Thao C., Nguyen T.X.,
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR308614; AR42802.1; -.
InterPro: IPR00329; Uteroglobin.
Fiam; PF010P9; Uteroglobin; 1.
SMART; SM00096; UTG; 1.
                                                                                                                                                                                                                                                                                                                                           2F5D641877EFD97E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6D34F9540C1FF742 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 IDGLQPMHKA------ELVKLLVQVLGSQDGAGTDYKDDD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                                                                                                                                                                                   16; Mismatches
                                                                                                                                                                                                                                                                                               PROSITE; PSO0028; ZINC_FINGER_C2H2_1; S. PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5. PNO-LING PROBING; Metal-binding; Zinc-finger. SEQUENCE 457 AA; 53091 MW; ZF5064187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSCIDGLQPMHKAELVKLLVQVL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9762 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 27.79
Matches 23; Conservative
                                                                                                                                                                                                                                                                                     ZnF_C2H2;
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 27.2% nes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 AA;
                                                                                                                  STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lipophilin AL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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248 CQMMPGMLLEQNPQFLYDNPSIFVIGILNLPLKVSPVELYNEFSNHGHILGVAINQSINE 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                       Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
Submitted (AuG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ALIO9739; CAB52270.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.5%; Score 73; DB 3; Length 609; 23.5%; Pred. No. 17; tive 20; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005543; AAH05543.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             HSSF; F13337, 2332.
InterPro; IPR000554; RRM_rec_mot.
InterPro; IPR003555; RRM_2.
Pfam; PF00076; rrm; 3.
SMART; SM00360; RRM; 2.
SMART; SM00362; RRM_2; 1.
PROSITE; PS50102; RRM; 2.
PROSITE: PS00030; RRM_RNP_1; 1.
SEQUENCE 609 AA; 68547 MW; 0ADE9A51603ABBF3 CRC64;
                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ol-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to signal recognition particle 54 kDa.
SRP54.
                                                                                               (TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 DMTHYAEVAVSTYESCIEIIEKFHAIAYEGSILQLFIK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 D----AKAAMTELKSCIDGLQPMH----KAELVKLLVQ 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200
                                                                           (TrEMBLrel. 13, Created)
                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, 007347, 2FFH.
HSSP, 007347, 2FFH.
MGD: MGI:1346687; SFP54.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR000897; SRP54.
InterPro; IPR004125; SRP54_SPB.
                                                                                                                                  Putative RNA-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02978; SRP_SPB; 1
ProDom; PD000819; SRP54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00448; SRP54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                              Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                NCBI_TaxID=4896
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                                                                                                                                                                                                                                                                                                       STRAIN=972H-;
                                                                           01-MAY-2000
                                                                                               01-MAY-2000
01-JUN-2002
                                                                                                                                                        SPAC343.07
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                                      Q9UT83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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RESULT 9
Q9UT83
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RA Adams N.D., Centiker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Scherer S.E., Holf W., Hoskins R.A., Galle R.E.,
RA George R.A. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeitfer B.D.,
RA Brandon R.C., Boyle C., Batter E.G., Helt G., Nalson C.R., Mixlos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bosley E.M.,
Beson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bosley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Geblos B., Delcher A., Deng Z., Mays A.D., Dew I., Ditez S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabrielian A.E., Garraz C., Ferriera S., Fielschmann W.,
RA Fosler C., Gabrielian A.E., Garraz C., Ferriera S., Fielschmann M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez JR., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Meil M.-H., Tbegwam C.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Alali M., Malush R., Murphy B., Murphy L., Murphy D., Mosler B., Shen H.,
Rako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Lasko P., Lei Y., Murphy B., Murphy L., Murphy D., Mosler E., Shen H.,
Rako D., R., Rocko C., Stapleton M., Strong R., Shen H.,
She Bazzolo M., Pittman G.S., Pan S., Pollart V., Schoeler E., Shen H.,
She Spier E., Spradling A.C., Stapleton M., Strong R., Shen H.,
Sheng R.C., Siden-Klamos I., Simpson M., Strong R., Shen H.,
Shings R., Teccor C., Thur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                           24 EDNDEF --- FMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAE 80
                                                                                                                                                                                                                                                                                             14.0%; Score 76; DB 16; Length 2104; 29.0%; Pred. No. 38; 1ve 10; Mismatches 34; Indels 2;
                                                                                                                                                                                                            Complete proteome. SEQUENCE 2104 AA; 236010 MW; 5FE345659599EED7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CG7928 protein (LD15405p).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 LVKLLVQVLGSO------DGAGTDYKDDDD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000421; FA58_C.
InterPro; IPR003961; FN_III.
Pfam: PP00074; FS_EP8_Lype_C; 1.
Pfam: PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
PROSITE: PS00018; EF_HAND; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                    27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                             Query Match
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Q9VAB8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 KGGGALSAVAATKSPIIFIGTGEHIDDFEPFKTQPFISKLLGMGDIEGLID-----KVN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KGSRALLLVALTLFCICRMATGEDNDEF----FMDFLQTLL-VGTPEELYEGTLGKYNVN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H., "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                              Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
14.1%; Score 76.5; DB 11; Length 504;
Best Local Similarity 32.4%; Pred. No. 5.5;
Matches 36; Conservative 16; Mismatches 40; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmioutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSQDGAGTDY 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg k.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK011928; BAB27921.1; -.
EMBL; BC019683; AAH19683.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM0382; AAA; 1.
PROSITE; PS00300; SRP54; 1.
SEQUENCE 504 AA; 55720 MW; 79AD58BE6DIE89CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TTEMBLrel. 20, Created)
01-MAR-2002 (TTEMBLrel. 20, Last sequence update)
01-JUN-2002 (TTEMBLrel. 21, Last annotation update)
Probable alpha-N-acetylgluçosaminidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002)
EMBL; AP003188; BAB80572.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 2104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR003593; AAA_ATPase.
InterPro: IPR000897; SRP54.
InterPro: IPR004125; SRP54_SPB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00448; SRP54; 1.
Pfam; PF02881; SRP54_N; 1.
Pfam; PF02978; SRP_SPB; 1.
ProDom; PD000819; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1346087; Srp54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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STRAIN=13 / TYPE A;
Pubmed=11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.;
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Strausberg R.

ISSP;

flesh-eater.";

DE REPARENTE DE LA PROPERTIE D

Q8XM24; **08XM24**

RESULT 6 **Q8XM24**

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SCIDGLQPMHKAELVKL----LVQVLGSQD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                     RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gutierrez-Sagal R., Nieto A.; "Cloning hamster uteroglobin/clara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LLVALTLFCICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELK 67
                                                     Rattus rattus (Black rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            1 MKGSRALLLVALTLFCICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-FISCHER; TISSUB-OLFACTORY EPITHELIUM;
MEDLINE-92007724; PubMed-1915264;
MEDLINE-92007724; PubMed-1915264;
Mober T.N., Boehm T., Keverne E.B., Rabbitts T.H.;
"Novel genes for potential ligand-binding proteins in subregions of the olfactory mucosa.";
EMBO J. 10:2813-2819(1991).
EMBL, X60661; CAA43068.1; -
InterPro; IRPR000329; Uteroglobin.
SEMART; SM00096; UTG; 1.
SEQUENCE 94 AA; 10401 MW; 25A4BBBB4977E247 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
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                                                                                                                                                                                                                                                                                                                                           DB 11; Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 96;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell 10 kDa protein.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: 137041; AAL31349.1;
InterPro; IPR003628; Uteroglbn_sub.
InterPro; IPR00329; Uteroglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5EB9CBDD46143389 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Potential ligand-binding protein.
                                                                                                                                                                                                                                                                                                                                      Ouery Match

64.5%; Score 349.5; DB 11;
Best Local Similarity 75.3%; Pred. No. 3e-31;
Matches 70; Conservative 11; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.7%; Score 90.5; DB 11;
27.8%; Pred. No. 0.019;
ative 17; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00404; UTEROGLOBIN_2; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AAMTELKSCIDGLQPMHKAELVKLLVQVLGSQD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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ProDom; PD012475; Uteroglbn_sub; 1.
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96 AA; 10509 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21, CC10 protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
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                                                                                                         NCBI_TaxID=10117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00096;
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238 TLKDTDKFSNEFSDFISRCLVKNPEERMSATALLQHKFIKSAK-PVAVLK------ 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J; TISSUE=EMBRYO;
MEDLINE=21085660; Pubmed=11217881;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular evolution of the Metazoan protein kinase C multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Porifera, Demospongiae, Tetractinomorpha,
Hadromerida, Suberitidae, Suberites,
NCBI_TaxID=55567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 478;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-96394688; PubMed-8798342;
Kruse M., Gamulin V., Cetkovic H., Pancer Z., Mueller I.M.,
Mueller W.E.G.;
Mueller W.E.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                          Mueller W.E.G.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 478 AA; 54098 MW; 6B38FF5FDB8D6332 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
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54 kDa.
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Last annotation update)
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Pred. No. 0.31;
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                                                                                                               478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Mismatches
                                                                                                                                                                                                             Stress-responsive protein kinase (PRKSD).
Suberites domuncula (Sponge).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 --ELIQDAMRILEEEGSGSDEEDDND 311
                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created) 01-AUG-1998 (TrEMBLrel. 07, Last sequinamar-2002 (TrEMBLrel. 20, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 KAELVKLLVQVLGSQDGAGTDYKDDDD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family.";
J. Mol. Evol. 43:374-383(1996).
JEBL: X13101; CAA73555.1;
HSSP; P24941; IHCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.1%;
31.0%;
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 14, 2003, 10:50:14 ; Search time 33 Seconds (without alignments) . 655.604 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-768-826-47 542 1 MKGSRALLLVALTLFCICRM.....VQVLGSQDGAGTDYKDDDDK 105

Scoring table:

671580 seqs, 206047115 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

671580

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_fung1:*
sp_human:*
sp_invertebrate:* sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_organelle:* sp_phage:* sp_plant:* SPTREMBL_21:* sb_mhc:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rvirus:* sp_bacteriap:*

sp_archeap:*

SUMMARIES

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Result		Query	Query			
NO.	Score	Match	Length	DB	ID	Description
7	477	0 88			OBBD33	
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7		17.0	7100	7	P8/112	P87112 schizosacch

O95247 homo sapien O95277 homo sapien Q9uig0 homo sapien O81081 human parai Q8ty89 methanopyru	F 3	013450 saccharomyc 080740 arabidopsis 080795 brucella me 081719 oryza sativ 085808 borrelia bu	P94238 borrella bu Q44978 borrella bu Q951y6 macaca fasc Q93k65 oryctolagus O5742 pyrococcus Q95844 mustella vis	O62006 branchiosto O86653 streptomyce O3561 mus musculu P97790 mus musculu P97789 mus musculu O99666 oryctolagus Q97c56 thermoplasm Q9bps1 bombyx mori
095247 095277 0901G0 081081 08TY89		013450 080740 08YCG5 Q8RYJ9 085808	P94238 Q44978 Q95JY6 Q9GK65 O57942 Q9XSW4	062006 086653 035651 P97790 P97789 Q9GK66 Q97C56
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ALIGNMENTS

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fibronectin-binding protein (imported) - Lactococcus lactis subsp. lactis (strain IL1403
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                             Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Walarme, K.; Weissenbach, J.; Ehrli anome Res. 11, 731-753, 2001
Title: The complete genome sequence of the lactic acid bacterium Lactocococus lactis ss Reference number: A86625; MUID:21235186; PMID:11337471
Accession: G86790
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A; Cross-references: GB:AE005176; PID:g12724308; PIDN:AAK05425.1; GSPDB:GN00146
A; Experimental source: strain IL1403
C; Genetics:
A; Gene: yngB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 DNDEFFM---DFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQP-MHKAE 80
                          Gaps
                                                                                              3;
                                                                 44 ELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGSQDGAG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69; DB 2; Length 540;
Pred. No. 25;
9; Mismatches 37; Indels:
                   Indels
Best Local Similarity 32.1%; Pred. No. 1.2e+02; Matches .17; Conservative 14; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.7%;
Best Local Similarity 30.6%;
Matches 22; Conservative
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354 KLKQAVKFLGEQ 365
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Search completed: May 14, 2003, 10:53:02 Job time: 19 secs

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Gaps

28;

Indels

27;

d. No. 11; Mismatches

Pred.

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23.5%; Pre-
       Similarity 23.5
23; Conservative
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A; Residues: 1-2458 <NOW>
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 27; Conser
                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-423 < PRO>
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          Loca1
        Best Loca
Matches
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                                                                                          28
                                                                                                                 308
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                                             A; Molecule type: mRNA
A; Residues: 1-42, 'DV', 45-504 <BER2>
A; Cross-references: EMBL:X16319; NID:954193; PIDN:CAA34386.1; PID:954194
C; Superfamily: signal recognition particle 54K protein
F; 2-504/Product: signal recognition particle 54K protein #status predicted <MAT>
                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9:
                                                                                                                                                                                                                                                                                                         Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                   Gaps
                                                                                                                                                                    2 KGSRALLLVALTLFCICRMATGEDNDEF----FMDFLQTLL-VGTPEELYEGTLGKYNVN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KGSRALLLVALTLFCICRMATGEDNDEF----FMDFLQTLL-VGTPEELYEGTLGKYNVN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                       DB 2; Length 504;
                                                                                                                                                                                                                                Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSQDGAGTDY 99
                                                                                                                                                 Indels
                                                                                                                                                                                                                 57 E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSQDGAGTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; I
                                                                                                                                                 40;
R;Bernstein, H.
Submitted to the EMBL Data Library, November 1989
A;Reference number: S14553
                                                                                                                      Query Match
14.1%; Score 76.5; Di
Best Local Similarity 32.4%; Pred. No. 3.7;
Matches 36; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.1%; Score 76.5; DF 32.4%; Pred. No. 3.7; ive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 73;
                                                                                                                                                                                                                                                                                                   SRP 54 protein - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 32.43
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 1
A; Introns: 44/1; 96/2; 325/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: SPDB:SPAC343.07
                                     A; Accession: S14553
                                                                                                                                                                                                                                                                            RESULT 11
S54143
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mannose-6-phosphate isomerase (EC 5.3.1.8) - human
N.Alternate names: phosphomannose isomerase
C.Species: Homo saplens (man)
C.Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999
C.Accession: S41122; S3866
E.P. Turcatti, G.; Wells, T.N.C.; Payton, M.A.; Smith, D.J.
Eur. J. Blochem. 219, 415-423, 1994
A.Title: Purification, cDNA cloning and heterologous expression of human phosphomanno
A.Reference number: S41122; MuID:94139717; PMID:8307007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: pltB
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acyl carrier pro
C;Keywords: carrier protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Pseudomonas fluorescens
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Nov-2000
                                                      248 COMMPGMLLEQNPQFLYDNPSIFVIGILNLPLKVSPVELYNEFSNHGHILGVAINQSINE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X76057; NID:g416016; PIDN:CAA53657.1; PID:g416017 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LLVALTLF-CICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLG-----KYNVNEDA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Nowak-Thompson, B.; Chaney, N.; Wing, J.S.; Gould, S.J.; Loper, J.E. J. Bacteriol. 181, 2166-2174, 1999
A;Title: Characterization of the pyoluteorin biosynthetic gene cluster A;Reference number: 218776; MUID:99194726; PMID:10094695
A;Accession: T17420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable polyketide synthase type I - Pseudomonas fluorescens
C.Species: Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 KAAMTELKSCIDGLQPMHK --- AELVKLLVQVLGSQDGAGTDYKD 101
18 CRMATG---EDNDEFFMDFLQTLLVG-----TPEELYE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                              | |: |:: :|||: :: | :::| :: | DMTHYAEVAVSTYESCIEIIEKFHAIAYEGSILQLFIK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Cross-references: GDB:119397; OMIM:154550
A:Map position: 15q22-15qter
C.Superfamily: yeast mannose-6-phosphate isomerase
C.Keywords: intramolecular oxidoreductase; isomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 70.5; DB
Pred. No. 13;
19; Mismatches
                                                                                                            D----AKAAMTELKSCIDGLQPMH----KAELVKLLVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.0%;
25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Conservative
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Length 2458;

DB 2;

Score 69.5;

12.8%;

Query Match

Length 609;

3

DB

13.5%;

Query Match

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Cipperies: Canis lupus familiaris (dog)
Cipate: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Feb-2001
Cipate: 07-Sep-1990 #sequence_revision 05-Feb-2001
Cipate: 07-Sep-1990 #sequence recognition particle, docking protein and A; Residues: 05-197; MUID:89330596; PMID:2502717
A; Molecule type: mRNA
A; Residues: 1-504 <ROE>
A; Mole: part of this sequence, including the amino end of the mature protein, was con A; Note: part of this sequence, including the amino end of the mature protein, was con A; Note: part of this sequence recognition from amino-acid sequence of 54K subuni A; Reference number: S05198; MUID:89330597; PMID:2502718
                A;Molecule type: DNA
A;Residues: 1-113 <RAY>
C;Comment: This protein is the major secretory product of the Clara cell and binds to C;Superfamily: uteroglobin
F;73/Region: ochre stop codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Title: Model for signal sequence recognition from amino-acid sequence of 54K subuni
A:Reference number: S05198; MUID:89330597; PMID:2502718
A:Accession: S05198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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A; Residues: 2-35;58-70;120-126;141-153;374-388;416-426;470-485 <BER>
C; Superfamily: signal recognition particle 54K protein
C; Keywords: GTP binding; nucleotide binding; P-loop
F;1-504/Product: signal recognition particle 54K protein #status experimental
F;108-115/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signal recognition particle 54K protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C;Accession: S05198; S14553
R;Bernstein, H.D.; Poritz, M.A.; Strub, K.; Hoben, P.J.; Brenner, S.; Walter
Nature 340, 482-486, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255 KGGGALSAVAATKSPIIFIGTGEHIDDFEPFKTQPFISKLLGMGDIEGLID-----KVN 308
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                             2 KGSRALLLVALTLFCICRMATGEDNDEF----FMDFLQTLL-VGTPEELYEGTLGKYNVN 56
                                                                                                                                                                                                                                                                                                                          6 ALLLVALTLFCICRMATGEDND -- EFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
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                                                                                                                                                                                                      Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 E----DAKAAMTELKSCIDGLQPMHK--AELVKL--LVQVLGSQDGAGTDY 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40; Indels
                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                Score 78.5; DB; Pred. No. 0.43; 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.1%; Score 76.5; DE 32.4%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              signal recognition particle 54K protein - dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 TOLKRLVDTLPQETRINIMKLTEKILTS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                             64 TELKSCIDGLOPMHKAELVKLLVQVLGS 91
                                                                                                                                                                                                14.5%;
30.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 32.4%;
Matches 36; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-504 <BER1>
A; Cross-references: EMBL:X16319
                                                                                                                                                                                      Query Match
Best Local Similarity 30.79
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S10619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96
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C;Species: Mus musculus (house mouse)
C;Species: S7-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C;Accession: JC2026
R;Ray, M.K.; Magdaleno, S.; O'Malley, B.W.; DeMayo, F.J.
Biochem. Biophys. Res. Commun. 197, 163-171, 1993
A;Title: Cloning and characterization of the mouse clara cell specific 10 kDa protein A;Reference number: JC2026; MUID:94071937; PMID:7916613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKGSRALLLVALTLFC----ICRMATGEDNDEFFMDFLQTLLVGTPEBLYFGTLGKYN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 ITITVVMLSICCSSASSDICPGFLQVLEALLMES-ESGYVASLKPFNPGSDLGNAGTQLK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID: 9164247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cony coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Userson uteroglobin precursor - brown hare
N.Alternate names: blastokinin
C.Specias: Lepus capensis (brown hare)
C.Specias: Lepus capensis (brown hare)
C.Specias: Lepus capensis (brown hare)
C.Accession: A23825
R.Lopez de Haro, M.S.; Nleto, A.
Blochem. J. 235, 895-898, 1898, 1898
A.Filte: Nucleotide and derived amino acid sequences of a cDNA coc Areference number: A23825; MUID:86323069; PMID:3019311
A.Reference number: A23825; MUID:86323069; PMID:3019311
A.Residues: 1-91 < LOP>
A.Residues: 1-91 < LOP>
A.Residues: 1-91 < LOP>
A.Residues: Ung
C.Comment: Uteroglobin, synthesized in the uterus and lung, is second bung; steroid binding; uterus
C.Superfamily: uteroglobin
C.Keywords: lung; steroid binding; uterus
C.Superfamily: uteroglobin #status predicted <SIG>
F.22-91/Product: uteroglobin #status predicted <AMT>
F.24/Disulfide bonds: interchain (to 90) #status predicted
F:90/Disulfide bonds: interchain (to 24) #status predicted
                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 26.2%; Pred. No. 0.17;
Matches 22; Conservative 19; Mismatches 42; Indels'
                                                                                                                                                                                                                                                                                                                                                                       0.17;
ches 42; Indel's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.7
44
77
4.7
                                                            Aintrons: 19/1; 81/3
C:Complex: homodimer linked by two disulfide bonds
C:Complex: homodimer linked by two disulfide bonds
C:Superfamily: uteroglobin
C:Keywords: lung; steroid binding; uterus
F:1-19/Domain: signal sequence #status predicted <AIC>
F:20-96/Product: uteroglobin #status predicted <AMT>
F:24/Disulfide bonds: interchain (to 90) #status predicted
F:90/Disulfide bonds: interchain (to 24) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length [51]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Mismatches 37; Indels
A:Cross-references: GB:L04503; NID:g202313; PIDN:AAA03625;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.8%; Score 80; DB 1; 26.8%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 VNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 SCIDGLQPMHKAELVKLLVQVLGS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 RLVDTLPQETRINIMKLTEKILTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell specific 10K protein - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 26.8% Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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us-09-768-826-47.rpr

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A; Molecule type: DNA
A; Residues: 1-96 <STR>
A; Cross-references: GB:L24372; NID:q461147; PIDN:AAA65446.1; PID:q785054
B; Sindy, G.; Katyal, S.L.; Brown, W.E.; Kennedy, A.L.
Exp. Lung Res. 19, 67-75, 1993
A; Title: Mouse Clara cell 10-kba (CC10) protein: cDNA nucleotide sequence and molecul
A; Reference number: A56656; MUID:93178380; PMID:8440203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A;Residues: 53-66,'NT',69-72 <AT2>
A;Cross-references: GB:M25038; NID:q165804; PIDN:AAA31499.1; PID:g165805
C;Comment: Uteroglobin is secreted by the uterus upon induction by progesterone. It b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uteroglobin precursor - mouse

N;Alternate names: CC10; Clara cell 10K protein precursor; Clara cell secretory prote
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 21-Jan-1997 #text_change 22-Jun-1999
C;Accession: A53025; A56656; I51925; S24783
R;Stripp, B.R.; Huffman, J.A.; Bohinski, R.J.
Genomics 20, 27-35, 1994
A;Tile: Structure and regulation of the murine Clara cell secretory protein gene.
A;Reference number: A53025; MUID:94292183; PMID:8020953
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A, Note: sequence extracted from NCBI backbone (NCBIP.1126148)
A, Note: sequence extracted from NCBI backbone (NCBIP.1126148)
A, Note: parts of this sequence, including the amino end of the mature protein, were c
R; Margraf, L.R.; Finegold, M.J.; Stanley, L.A.; Major, A.; Nawkins, H.K.; DeMayo, F.J
Am. J. Respir. Cell MOL. Biol. 9, 231-238, 1993
A, Title: Cloning and tissue-specific expression of the cDNA for the mouse Clara cell
A; Reference number: 151925; MUID:94000840; PMID:8398159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLAITLALVILALLCSPASAGICPR------FAHVIENLLGTPSS-YETSLKEFE 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKGSRALLLVALTLFC----ICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYN 54
                                                                                                                                                                                       A)Cross-references: GB.M32012; NID:g165807; PIDN:AAA31500.1; PID:g165809 R:Atger, M.; Perricaudet, M.; Tiollais, P.; Milgrom, E. Blochem. Biophys. Res. Commun. 93, 1082-1088, 1980 A;Title: Bacterial cloning of the rabbit uteroglobin structural gene. A;Reference number: I46906; MUID:80241888; PMID:6156676 A;Accession: I46906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA; protein
A;Residues: 1-96 <SIN>
A;Cross-references: EMBL:X67702; NID:949690; PIDN:CAA47936.1; PID:949691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: uteroglobin
C; Keywords: homodimer; steroid binding; uterus
F;1-21/Domain: signal sequence #status experimental <SIG>
F;2-91/Product: uteroglobin #status experimental <MAT>
F;24/Disulfide bonds: interchain (to 90) #status experimental
F;90/Disulfide bonds: interchain (to 24) #status experimental
                                                  Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: mRNA
A;Residues: 1-96 <RES>
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C:Complex: homodimer linked by two disulfide bonds
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                                                                                                A; Molecule type: DNA
A; Residues: 1-45,'V',47-91 <SU2>
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A. Accession A9828.

A. Molecule type: protein
A. Molecule to the Brookhave Protein Data Bank, April 1989
A. Molecule to the Brookhave Protein
A. Molecule to the Brookhave Totalography, 1.34 angstroms
A. Molecule to the Brookhave Totalography, 1.34 angstroms
A. Molecule to the Brookhave Totalography, 1.34 angstroms
A. Meference number: A8652; MUD: 88011213; MMD: 3656405
A. Contents: annotation; X-ray crystallography, 1.34 angstroms
A. Meference number: A8652; MUD: 88199637; MMD: 3704039
A. Contents: annotation; X-ray crystallography, 1.64 angstroms; residues 22-91
A. Mol. Biol. 206, 153-170, 1989
A. Title: Structure and refinement of the oxidized P2-1 form of uteroglobin at 1.64 angst
A. Mol. Biol. 206, 153-170, 1989
A. Title: Structure and refinement of the oxidized P2-1 form of uteroglobin at 1.64 angst
A. Melne, C. S. Suske, G.; Arnemann, J.; Menz, M.; Cato, A.C.B.; Beato, M.
A. Melne, C. S. Suske, G.; Arnemann, J.; Menz, M.; Cato, A.C.B.; Beato, M.
A. M. Melecence number: 146904; MUD: 83014990; PMID: 6956897
A. M. Melecence number: Insolation and structure of the gene for the progesterone-inducible protein uter
A. McCession: I46904
A. Molecule type: protein and A. Molecule to the gene for the gene for the gene for the A. Molecule type and A. Molecule to the gene for the gene for the A. Molecule type and A. Molecule to the gene for the gene for the gene for the A. Molecule type to the gene for the gene for the A. Molecule type to the gene for the decompla
                                                                       A; Residues: 22-91 < LOP>
A; Experimental source: lung
B; Atger, M; Mercier, J.C.; Haze, G.; Fridlansky, F.; Milgrom, E.
B; Atger, M.; Mercier, J.C.; Haze, G.; Fridlansky, F.; Milgrom, E.
B; Accession: 400303; MUID: 79187160; PMID: 571719
A; Reference number: A00303; MUID: 79187160; PMID: 571719
A; Recent at A00303
A; Molecule type: protein
A; Residues: 1-5, F', 7-10, X', 15, G', 17-54, X', 56, 'B', 58-66, 'B', 68-70, 'XX', 73 < ATG>
A; Molecule type: protein
A; Residues: 1-5, F', 7-10, A', 15, G', 17-54, X', 56, 'B', 58-66, 'B', 68-70, 'XX', 73 < ATG>
A; Molecule type: protein
A; Reference number: A90417; MUID: 79042086; PMID: 568483
A; Title: Amino acid sequence of progesterone-induced rabbit uteroglobin.
A; Residues: 22-81, 'Q', 83-91 < PON>
A; Reference number: A93824; MUID: 79074850; PMID: 281700
A; Arcession: A03824; MUID: 79074850; PMID: 281700
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A; Reference number: A24217; MUID:86056319; PMID:2415398
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A; Residues: 39-77 <CH2>
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A; Residues: 1-91 <MEN>
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uteroglobin precursor [validated] - rabbit
N;Alternate names: blastokinin
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Feb-1980 #sequence_revision 15-Oct-1982 #text_change 15-Sep-2000
C;Accession: A92391; A93461; A90935; A24217; A90303; A90417; A93824; A94608; I46904;
R;Ballly, A.; Atger, M.; Atger, P.; Cerbon, M.A.; Allzon, M.; Vu Hai, M.T.; Logeat, F
J; Biol. Chem. 258, 10384-10389, 1983
A;Title: The rabbit uteroglobin gene. Structure and interaction with the progesterone A;Reference number: A92391; MUID:83290960; PMID:6309802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEBS Lett. 376, 257-261, 1995
A; Title: Cloning of a Syrian hamster CDNA related to sexual dimorphism: establishment
A; Reference number: S68231; MUID:96105393; PMID:7498554
A; Accession: S68231
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A:Title: Primary structure of rabbit lung uteroglobin as deduced from the nucleotide
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A;Residues: 1-91 ABAI>
A;Cross-references: GB:K00049; NID:g165789
R;Suske, G; Wenz, M.; Cato, A.C.B.; Beato, M.
Nucleic Acids Res. 11, 2257-2271, 1983
A;Fitle: The uteroglobin gene region: hormonal regulation, repetitive elements and
A;Reference number: A93461; MUID:83220783; PMID:6304644
                                                                                                                                                                                                                                                                                                                              FHG22 protein precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Aug-1998
C;Accession: S68231
R;Dominguez, P.
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A;Residues: 1-91 <CHA>
A;Cross-references: GB:K01657; NID:g165794; PIDN:AAA31497.1; PID:g165795
R;Lopez de Haro, M.S.; Nieto, A
FEBS Lett. 193, 247-249, 1985
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R;Chandra, T.; Bullock, D.W.; Woo, S.L.C.
DNA 1, 19-26, 1981
--- PSFORVIETLIMDIPSS-YEAAMELFS
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C;Superfamily: uteroglobin
E5:1-21/Domain: signal sequence #status predicted <SIG>
F;22-95/Product: FHG22 protein #status predicted <MAT>
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                                                                                                                                               87
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51 PDQDMREAGAQLKKLVDTLPQKPRESIIKLMEKIAQS
                                                                       55 VNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGS
MKLAVTLTLVTLALCCSSASAEIC-
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Matches 31; Conserv
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A; Residues: 1-91 <SUS>
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A; Molecule type: mRNA
A; Residues: 1-95 < DOM>
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A; Residues: 1-91 <SIN>
A; Cross-references: GB:X13197; NID:q23131; PIDN:CAA31584.1; PID:q23132
A; Accession: PS0309
A; Molecule type: protein
A; Residues: 22-23; X', 25-28, X', 30-31, X', 33-36 <SI2>
B; Bernard, A.; Roels, H.; Lauwerys, R.; Witters, R.; Gielens, C.; Soumillion, A.; Van Da
Clin. Chim. Acta 207, 239-249, 1992
A; Title: Human urinary protein 1: evidence for identity with the Clara cell protein and
A; Reference number: A56890; MUID:93009001; PMID:1395029
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A; Residues: 22-45 < BRR>
A; Residues: 22-45 < BRR>
A; Residues: 22-45 < BRR>
A; Experimental source: urine
A; Note: sequence extracted from NCBI backbone (NCBIP:119391)
B; Hay, J.G.; Danel, C.; Chu, C.; Crystal, R.G.
Am. J. Physiol. 268, 565-575, 1995
Am. J. Physiol. 268, 565-575, 1995
A; Title: Human CCIO gene expression in airway epithelium and subchromosomal locus sugges
A; Reference number: 138397
A; Accession: 138397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 31-War-1992 #sequence_revision 31-Mar-1992 #text_change 20-Aug-1999
C;Date: 31-War-1992 #sequence_revision 31-Mar-1992 #text_change 20-Aug-1999
C;Accession: J50036; Ps0309, A56890; I38397
R;Singh, G: Katyal, S.L.; Brown, W.E.; Philips, S.; Kennedy, A.L.; Anthony, J.; Squegli Biochim. Biophys. Acta 950, 329-337, 1988
A;Title: Anino-acid and cDNA nucleotide sequences of human Clara cell 10kDa protein.
A;Reference number: J50036; MUID:89000784; PMID:3167058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :Cross-references: EMBL:U01101; NID:9457932; PIDN:AAA81885.1; PID:9457933
:Comment: This protein consists of two identical polypeptides linked by two disulfide
                       A.Cross-references: EMBL:X51318; NID:955536; PIDN:CAA35701.1; PID:955537
K:Umland, T.C.: Swaminathan, S.; Furey, W.; Singh, G.; Pletcher, J.; Sax, M.
J. Mol. Biol. 224, 441-448, 1929
A;Title: Refined structure of rat clara cell 17 kDa protein at 3.0 A resolution.
A;Reference number: S21676; MUID:92219263; PMID:1560460
A;Reference number: S21676; MUID:92219263; PMID:1560460
C;Superfamily: uteroglobin (r. Tay crystallography, 3.0 angstroms
F;24/Disulfide bonds: interchain (to 90) #status experimental
F;90/Disulfide bonds: interchain (to 24) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S ITITVLMLSICCSSASSDICPGFLQVLEALLLGS-ESNYEAALKPFNPASDLQNAGTQLK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKGSRALLLVALTLFC----ICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LLVALTLFCICRMATGEDNDEFFMDFLQTLLVGTPEELYEGT5GKYNVNEDAKAAMTELK 67
                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 17.8%; Score 96.5; DB 2; Length 96; Best Local Similarity 29.8%; Pred. No. 0.0044; Matches 25; Conservative 17; Mismatches 41; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: uteroglobin
1-21/Domain: signal sequence #status predicted <SIG>
;22-91/Product: Clara cell 10K protein #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.0%; Score 92; DB 2; Length 91; 27.8%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clara cell 10% protein precursor - human N;Alternate names: urinary protein 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 SCIDGLQPMHKAELVKLLVQVLGS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 RLVDTLPQETRINIVKLTEKILTS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.8%;
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Residues: 1-91 <RES>
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8

SEQ. 1D NO. 18 47 AC NO: S17449; Database: PIR_73 us-09-768-826-47.rpr

GenCore version $5.1.4_p5_4578$: Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May 14, 2003, 10:50:34 ; Search time 17 Seconds Run on:

(without alignments) 593.771 Million cell updates/sec

US-09-768-826-47 542 1 MKGSRALLLVALTLFCICRM......VQVLGSQDGAGİDYKDDDDK 105 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
3: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable ligand-bi	polychloringted bi		protein p				cell specific 10K				probable RNA-bindi	mannose-6-phosphat	probable polyketid	fibronectin-bindin	t7i23.15 protein -	major allergen Fel	hypothetical prote	hypothetical prote	=	BNIl protein - yea	Ω	⊆	outer surface prot		ystatin		3C3.20c protein -	phosphodiesterase
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SUMMARIES		; ; ; ; ; ;																					•							
SUMM	ΩI		A36581	JS0036	S68231	UGRB	UGMS	UGRBL	JC2026	S05197	S05198	S54143	T38656	S41122	T17420	G86790	T38128	A56413	530947	T16137	C83075	S63244	T02269	AD3580	S70285	JC1136	A43644	A71243	T10929	T30244
	DB	7	~	~	7	-	-	Н	~	~	7	ď	~	~	7	~	~	~	~	~	~	~	~	7	7	~	7	7	7	~
	Length	94	96	91	95	91	96	91	113	504	504	504	609	423	2458	540	2100	92	270	299	322	1953	511	358	192	92	122	362	1321	1687
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dP	Query	64	17	17	7	16	15	14	14	14	14	14	3	13	12	12	12	12	12	12	12	12	12	12	17	12	12	12	12	12
	Score	349.5	96.5	92	91	88	81.5	80	-: &	76.5	76.5	ė.	73	٠	6	69	68.5	68	9	67.5		67.5	67	66.5	99	S.	65.5	S.	65.5	65.5
	Result No.	1		m	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

exoribonuclease, v	MG331 homolog P01	repressor modE hom	hypothetical prote	hypothetical prote	genome polyprotein	coA-liqase / coenz	hypothetical prote	tyrosine transamin	cytochrome P450-11	qene ULS protein -	hypothetical prote	H+-transporting AT	probable DNA repai	fusion, PTS system
T30175	873690	B64175	G71146	E96641	ZLNZP3	. E90436	B89808	XNRTY	H85440	WMBEUS	T20725	C69395	G81326	н96951
20	17	7	~	~	Н	~	~	Н	7	٦	7	-	~	7
1706	209	255	312	842	2233	339	403	454	518	882	190	342	446	627
12.1	12.0	12.0	12.0	12.0	12.0	11.9	11.9	11.9	11,9	11.9	11.8	11.8	11.8	11.8
65.5	65	65	65	65	65	64.5	64.5	64.5	64.5	64.5	64	64	64	64
30	32	33	34	32	36	37	38	6ε	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 S17449 Probable C; Specie C; Date: C; Access R; Dead A; Title: A; Recess A; Access A; A	RESULT 1 S17449 Stockers: Rattus norvegicus (Norway rat) C; Decies: Rattus norvegicus (Norway rat) C; Decies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 R; Dear, T.N.; Boehm, T.; Keverne, E.B.; Rabbitts, T.H. EMBO J. 10, 2813-2819, 1991 A; Reference number: S17447; MUID:92007724; PMID:1915264 A; Reference number: S17447; MUID:92007724; PMID:1915264 A; Returus: pre-liminary A; Residues: 1-94 < CDEA> A; Residues: 1-94 < CDEA> A; Cross-references: EMBL:X60661; NID:957735; PIDN:CAA43068.1; PID:957736
Que Bes Mat	Query Match 64.5%; Score 349.5; DB 2; Length 94; Best Local Similarity 75.3%; Pred. No. 7.3e-30; Matches 70; Conservative 11; Mismatches 11; Indels 1; Gaps 1;
Qy	1 MKGSRALLLVALTLECICRMATGEDNDEFFMDELQTLLVGTPEELYEGTLGKYNVNEDAK 60
Qy	61 AAMTELKSCIDGLQPWHKAELVKLLVQVLGSQD 93 :

polychlorinated biphenyl-binding protein precursor - rat
N.Alternate names: Clara cell 10K secretory protein
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 20-Aug-1999
C; Accession: A36581; S10185; S21676
R; Nordlund-Moeller, L.; Andersson, O.; Ahlgren, R.; Schilling, J.; Gillner, M.; Gusta J. Bol. Chem. 265, 12690-12693, 1990
A; Title: Cloning, Structure, and expression of a rat binding protein for polychlorina A; Reference number: A36581; MUID:90324266; PMID:2115524

A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-96 < NOR
A; Residues: 1-96 < NOR
A; Residues: 1-96 < NOR
A; Cross-references: GB:J05536; NID:g206039; PIDN:AAA41817.1; PID:g206040
A; Cross-references: GB:J05536; NID:g206039; PIDN:AAA41817.1; PID:g206040
B; Hagen, G: Wolf, M: Katyal, S.L.; Singh, G:; Beato, M.; Suske, G.
Nucleic Acids Res. 18, 2939-2946, 1990
A; Reference number: S10185; MUID:90272398; PMID:2349092
A; Accession: S10185
A; Actual translation not shown
A; Molecule type: DNA

Mon. May 19 15:09:12 2003

105) with: Standard Deviation 17.19 Results file 768826-47_x.res made by spaula on Wed 14 May 103 Total Elapsed 00:00:00:00 Results of the initial comparison of US-09-768-826447 File : r55778.seq File : x60661.seq Query sequence being compared:US-09-768-826-47 (1-105) Number of sequences searched: 12 Number of scores above cutoff: 12 ,: Joining penalty Window size SEARCH STATISTICS FastDB - Fast Pairwise Comparison of Sequences Release 5.4 Median 5 K-tuple 1690 12 12 PARAMETERS CPU 00:00:00.00 Unitary 6 1.00 0.05 0 Number of residues: Number of sequences searched: Number of scores above cutoff: Mean 9 > 0 < 0 | 0 IntelliGenetics > 0 < Similarity matrix Translation Frame Mismatch penalty Gap penalty Gap size penalty Cutoff score Randomization group SCORE 01 STDEV 0 Scores: Times:

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found

The list of best scores is:

Sequence Name	Description	E .		H	Length	Init. Score	Opt. Score	Sig.	Frame
x606	**** 3 TOIG of:	tandar 60661	devia	rt (ve m 145	an *** 64	* 70	3.20	-
9.5	of of		check:	tion fro 2527 2244	om mean 144 137	k .	21	0.1	
		x60661	check:	2527	143	າທະ	22	.00	
	TOIG OF:	x60661	check:	2527	144	ດທຸ	61.	200	
		r55778 r55778	check:	2244 2244	137 138	4 4	12 13	0.7	
10.	OIG	r55778 r55778	check:	2244 2244	138	44	16	-0.29	m 4
$\frac{11}{x60661}$	TOIG of: TOIG of:	r55778 x60661	check:	2244 2527	139 144	4 E	14 16	0.3	
1. US-09-768-826- x60661	47 (1-105) OIG of: x6	.0661 ch	check: 25;	27 from:	-	to: 435			
Initial Score Residue Identity Gaps Translation Frame	61 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Optimized)Matches Conservat:	ed Score	= stituti	70 71 ons	Significanco Mismatches	ance es	3.20	000
X MKGSRALLI VVTVMKGSSA-LI X 10	X 10 20 30 40 50 60 MKGSRALLLVALTLECICRMATGEDNDEFEMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKS 1111 111111 11111 1111 1111 1111 111	0 MATGEDND 11 LTRAEDDN 30	30 EFFMDFL(40 STLLVGTE STLLVGTE 40	PEELYEG	50 TLGKYN 11111 PLGKYN	60 VNEDAK? VNDMAK?	AAMTEI AALTEI	1 1 1 1 1 1 1 1 1 1
70 80 90 100 X CIDGLQPMHKAELVKLLVQVLGSQDGAGTDYKDDDDK	80 100 X PMHKAELVKLLVQVLGSQDGAGTDXKDDDDK	10 ODGAGTDY I QEDTXAAP	O X KDDDDK 	SNRTSRTE	3 20 CAR	TSASSF	VNSPSN	CXINK),XC
SP	0		1		0	7	5	7	
2. US-09-768-826 x60661	-47 (1-105) TOIG of: x6	1990	check: 25	27 from:	1	to: 435	2		
Initial Score Residue Identity Gaps Translation Fram	238	Optimized Matches Conservati	Sco	= ostitut	21 Si 26 Mi ions	lgnificance Ismatches	ance .	-0.1	000
		* 2	X MKGSRALLLVALTLFC	10 LVALTEFO	CIC	20 -RMATO	20 RMATGEDNDEFFMDFLQTL	O FMDFL	OTL
WTALDFIDLTVRGXIYWXRSTGLST 10 20	SXIYWXRSTGL 20	STSMATCT 30	SMATCTAGPIARRGQAMFWGCLCVLL 30 40 50	GOAMFWGO 40	SLCVLLS 50	тхнгн	SIXHLHQQLDQLLLMHRLQFI 60 70	LMHRL	OFI 0
40 50 LVGTPEELYEGTLG NAGLELCORCLG	50 60 70 EELYEGTLGKYNVNEDARAAMTELKSCIDGLQPMH	AAMTEL GPFIELFW	70 -KSCIDGL WGPHQECL 1	70 80 SCIDGLQPMHKAELV 	9C LVKLLVQVLG -EKLIVILCS	90 VLGSQI 11 11 11 120	90 100 X KLLVQVLGSQDGAGTDYKDDDDK 	TRDDDDK TEHGXSHQK 130 X	X HO X
SAAPFHDSH 140									
3. US-09-768-826 r55778	-47 (1-105) TOIG of: r5	5778	check: 22,	44 from	н 	to: 417	_		
Initial Score	ii N	Optimiz6	zed Score	11	15 S:	Significance	sance =	-0.2	8

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CDCHEREQRSSGGSNRALHLWADXSRGXOXVFHGIPANTPGGDPRALXRAPGQVQCQXHGGGSADRAQVLH
                                      ---LILFCICRMAT-GED-------NDEFFMDFLQTLL
                                                                                                                                                                                                       XXT----ADGPYTGQAAGASA-----RCSRGHISSPKTWL-DLCEQ----XDQPYTWPWMCXDQCFFTS 80 80 120 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X 10 20 30 40 50 MKGSRALLLVALTLFCICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPIFCRNGPNLPLSLKPXRAGLGXNQMGTLQTXGRPKAARNGVVTAXSBSPNPGPTWKGPGAL-GGEPPPWQ 10 20 60 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGSGSRHTTAVLGRRGLERGQGTAPRIAREVAHRPVPRGPSRSGRGLEKGFKRSRPRSLQPL----AFLMSG
50 60 70 80 90 x 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 40 90 90 GEDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGSQDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FFLTFTNIVLLSPG-QNAAF-----TTEENGASCGGKGSCGWEHREAXAQDPGTPQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 20 30 40 50 60 MKGSRALLLVALTLECICRMATGEDNDEFEMDFLOTLLVGTPEELYEGTIGK-YNVNEDAKA-A-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNEDAKAAMTELKS-----CIDGL---QPM-HKAELVKL------LVQVLGSQDGAGTDYKDDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 Optimized Score = 13 Significance = -0.29
27% Matches = 19 Mismatches = 28
2 Conservative Substitutions = 0
                                                                                                                                          40 50 60 100 X VGTPEELYEGTLGKYNVNEDAKAAMTELKSCIDGLQPMHKAELVKLLVQVLGSQDGAGTDYKDDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSVPSPALARGLFSPAPLMCAGILSLGLPMFPPAXSLPATRCSVFFRCECRVLSWXQENNVGERQK
80 100 100 110 120 130 x
                                                                                                                                                                                                                                                                                                                                                        7. US-09-768-826-47 (1-105)
r55778 TOIG of: r55778 check: 2244 from: 1 to: 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-768-826-47 (1-105)
r55778 TOIG of: r55778 check: 2244 from: 1 to: 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9. US-09-768-826-47 (1-105)
r55778 TOIG of: r55778 check: 2244 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                            Optimized Score = 12
Matches = 18
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Optimized Score = 15
Matches = 23
Conservative Substitutions
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MKGS-RALLLVA-
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21
51
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25
3
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Residue Identity =
Gaps
Translation Frame=
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Residue Identity = Gaps
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                                                                                                                                                                                                                                                                      LQIPARPGRAPCHWA--VSHLPGNSRCRPLPSLEASSPÜHRCGVPGSXAXASRCSHPHDPFPPHDAPFSSVV 60 60 100 110
                                                                                                                                                 TRF---SVETG----QIFPYPXNPKGQGWAEIKWEPSRHK----EGORLOGTGSXPLKSL
X 30 40
                                                                                          10 x 20 30 40 50 60 MKGSRALLLVALTLECICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYNVNEDAKAAMT---ELKS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X 10 20 30 60
MKGSRALLLY-ALTLECICRMATGEDNDEFFMDFLQTLLVGTPEELXEGTLGKYNVNEDAKAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCIRLYXFNSSRVNLLVKKHWSXHİHGHVYGWSYCSQRSSHVLGLL-MCFLEHLALAPAAXPVAPYABAAVH
10 50 60 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OCRTXALSALPWPCHXHCTCPGALHRALIGSPPGVFAGIPXKTHCHPLLXSAHRCRARLEPPEERCSLSXQS
100 110 120 130 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLHXTLLIXQFEGEFTGEEALVLAHPWPRVRLVLLLAE-VKPCFGAAYVSSXASSTCTSSLTSCSL
X 10 20 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCSSSMQDLSSVSÅALAMSLTLYLPRGPSXSSGVPTRSVCRNSMKNSLSSSALVSPQMOSTVRATRAL
70 80 120. 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X 10 20 30 40 50 60 MKGSRALLLVALTLECICRMATGEDNDEFEMDELLVGTPEELYEGTLGKYNVNEDAKAAMT-ELKSC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Significance - 0.23
Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 Optimized Score = 18 Significance = -0.23
19% Matches = 22 Mismatches = 76
15 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 Optimized Score - 19 Significance - -0.23
21% Matches - 28 Mismatches - 62
39 Conservative Substitutions - 0
3
         Matches - 24 Mismatches Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5. US-09-768-826-47 (1-105)
x60661 TOIG of: x60661 check: 2527 from: 1 to: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to:: 435
                                                                                                                                                                                                                       70 80 90 100 X ----CIDGLQPMHKAELVKLL----VQVLGS------QDGAGTDYKDDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                     4. US-09-768-826-47 (1-105)
x60661 TOIG of: x60661 check: 2527 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 Optimized Score - 22
23% Matches - 26
8 Conservative Substitutions
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6. US-09-768-826-47 (1-105)
x60661 TOIG of: x60661 check: 2527 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 80 90 100 X
--MTELKSCIDGLQPMHKAELVKLLVQVLGSQDG--AGTDYKDDDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 80 100 X
-----IDGLQPMHKAELVKLLVQVL-----GSQDGAGTDYKDDDDK
      218
32
6
                                                                                                                                                                                                                                                                                                                                                      NAAFCPGDRRTMLVNVKK
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Initial Score
Residue Identity -
Gaps -
Translation Frame-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial Score
Residue Identity -
Gaps -
Translation Frame-
Residue Identity =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial Score
Residue Identity = Gaps
                               Gaps -- Translation Frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps -
Translation Frame-
```

Significance = -0.29
Mismatches = 81

X 10 20 MKGSRALÉLVALTLECICRMAT

Significance - -0.29
Mismatches - 60

LPFMTV

X DK t

20	SAQPCPLG		-0.29 47 0 20 FCICRMAT 1	OSDTAÖAFGSÖ	-0.29 68 0	60 VNEDAKAAMTELKSC LRIPAHISG	PNPALXGF 120		-0.35	KYNVNEDA RQRXQSSS
40	SLCLEGSHLI 110	to 417	Significance = -0.29 Mismatches = 47 s	80 ВМНКАЕТИКЦ	0.417 nificance marches	60 KYNVNEDAKA I I I I I I I I I I I I I I I I I I I	110 110 110	. 435	Significance Mismatches	50 PEELYEGTLG WASTMSMTWP
. 08	X K HDPVPCSLWP X 100	from: 1 to	10 Sign 12 Mism Lions : : X : X MKGS	GEO 70 80 90 90 GEO 70 BO BO 90 90 GEO GEO GEO GEO GEO GEO GEO GEO GEO GEO	Sig	40 50 1 50 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TPFLAAFGUP	from: 1 to:		40 SFLQ-TLLVGT VGPQKSSMKGF
20	100 X -AGTDYKDDDDK RAGIWRRALSGH	. 2244	Score = 10 12 ve Substitutions RGTGRXATSLASLGAV	60 IVNEDAKAAMT I I WXTSK	: 2244 ore = Substit	40 .QTLLVGT SORKKTEHRVA	i00 x QDGAGIDYKDDDDK QVGPGFGEGIXAVT' 90 x	2527	Score = 16 24 .ve Substitutions	30 GEDNDEFFMI SWNSCKHSWV
	90 LLVQVLGSQDG- 1 1 LTAQCPGALPGR 80	5) r55778 check	Optimized Scc Matches Conservative FSKARPDLEGPRG7	50 LYEGTLGKYN MPRSVLVTGEQC	1-105) of: r55778 check: 4 Optimized Scoil Matches 17 Conservative 9	x 20 30 40 50 50 FCICRMATGEDNDEFFMDFLQTLLVGTPEELYEGTLGKYN 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SQDGA 	(1-105) of: x60661 check:	Optimized Scc Matches Conservative	20 30 40 50 TLECICRMATGEDNDEFFMDFLQ-TLLVGTPEELYEGTLGKYNVNEDA
10	80 HKAELVK: RDLPGRW	v 7 (1-105) IG of: r59	4 198 3 4 4 GRDRLKP	40 LVGTPEE LRFLPLX 120		20 CICRMAT 1 FEXRSPT	90 LVQVLGS 1 12 70	7 (1-10 IG of:	3 168 41 2	L 1 1LXPCSAS 20
*	70 80 90 100 X -WTELKSCIDGLQPMHKAELVKLLVQVLGSQDG-AGTDYKDDDDK	FWGXGKIWPVXTENRV 130 10. US-09-768-826-47 (155778	Initial Score = 4 Optimized Score = 10 Significance = -0.29 Residue Identity = 19% Matches Gaps = 3 Conservative Substitutions 12 Mismatches = 47 Translation Frame = 4 GAPPDIRKARGCKERGRDRLKPFSKARPDLEGPRGTGRXATSLASLGAVPCPRSPERILLYALTLFCICRWAT 10 10 10 10 10 10 10 1	ч	11. US-09-768-826-47 r55778 TOIG Initial Score Residue Identity = Gaps Translation Frame=	. MKGSRALLLVALTLECICRMATGEDNDEFFMDFLQ- 1 1 1 1 1 1 1 1 1 1	TO 80 90 100 X IDGLOPMHKAELVKLLVQVLGSODGAGTDYKDDDDK	12. US-09-768-826-47 x60661 TOIG	Initial Score Residue Identity - Gaps Translation Frame-	X 10 50 MKGSRALLLVALTLFCICRMATGEDNDEFFMDFLQ-TLLVGTPEELYEGTLGKYNVNEDA 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1